

Sheng Ye

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

790
citations

840776

11
h-index

794594

19
g-index

20
all docs

20
docs citations

20
times ranked

1693
citing authors

#	ARTICLE	IF	CITATIONS
1	Junctional and somatic hypermutation-induced CX4C motif is critical for the recognition of a highly conserved epitope on HCV E2 by a human broadly neutralizing antibody. <i>Cellular and Molecular Immunology</i> , 2021, 18, 675-685.	10.5	10
2	The crystal structure of ORP3 reveals the conservative PI4P binding pattern. <i>Biochemical and Biophysical Research Communications</i> , 2020, 529, 1005-1010.	2.1	9
3	Crystal Structure of Refolding Fusion Core of Lassa Virus GP2 and Design of Lassa Virus Fusion Inhibitors. <i>Frontiers in Microbiology</i> , 2019, 10, 1829.	3.5	11
4	BubR1 phosphorylates CENP-E as a switch enabling the transition from lateral association to end-on capture of spindle microtubules. <i>Cell Research</i> , 2019, 29, 562-578.	12.0	46
5	Characterization by high-resolution crystal structure analysis of a triple-helix region of human collagen type III with potent cell adhesion activity. <i>Biochemical and Biophysical Research Communications</i> , 2019, 508, 1018-1023.	2.1	33
6	Munc18 and Munc13 serve as a functional template to orchestrate neuronal SNARE complex assembly. <i>Nature Communications</i> , 2019, 10, 69.	12.8	80
7	A critical epitope in CD147 facilitates memory CD4+ T-cell hyper-activation in rheumatoid arthritis. <i>Cellular and Molecular Immunology</i> , 2019, 16, 568-579.	10.5	25
8	Structure of Escherichia coli Arginyl-tRNA Synthetase in Complex with tRNAArg: Pivotal Role of the D-loop. <i>Journal of Molecular Biology</i> , 2018, 430, 1590-1606.	4.2	12
9	Structural basis of ligand binding modes at the neuropeptide YY1 receptor. <i>Nature</i> , 2018, 556, 520-524.	27.8	100
10	Structure of a prokaryotic SEFIR domain reveals two novel SEFIR-SEFIR interaction modes. <i>Journal of Structural Biology</i> , 2018, 203, 81-89.	2.8	4
11	Structure of the DNA-binding domain of human myelin-gene regulatory factor reveals its potential protein-DNA recognition mode. <i>Journal of Structural Biology</i> , 2018, 203, 170-178.	2.8	8
12	Structure of thrombospondin type 3 repeats in bacterial outer membrane protein A reveals its intra-repeat disulfide bond-dependent calcium-binding capability. <i>Cell Calcium</i> , 2017, 66, 78-89.	2.4	7
13	Creating an Artificial Tail Anchor as a Novel Strategy To Enhance the Potency of Peptide-Based HIV Fusion Inhibitors. <i>Journal of Virology</i> , 2017, 91, .	3.4	25
14	Rational improvement of gp41-targeting HIV-1 fusion inhibitors: an innovatively designed Ile-Asp-Leu tail with alternative conformations. <i>Scientific Reports</i> , 2016, 6, 31983.	3.3	12
15	Structure of iridoid synthase in complex with NADP + /8-oxogeranial reveals the structural basis of its substrate specificity. <i>Journal of Structural Biology</i> , 2016, 194, 224-230.	2.8	16
16	Improved Pharmacological and Structural Properties of HIV Fusion Inhibitor AP3 over Enfuvirtide: Highlighting Advantages of Artificial Peptide Strategy. <i>Scientific Reports</i> , 2015, 5, 13028.	3.3	33
17	Structure of a double-domain phosphagen kinase reveals an asymmetric arrangement of the tandem domains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 779-789.	2.5	3
18	Structure-based discovery of Middle East respiratory syndrome coronavirus fusion inhibitor. <i>Nature Communications</i> , 2014, 5, 3067.	12.8	324

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19	Crystal structure of kindlin-2 PH domain reveals a conformational transition for its membrane anchoring and regulation of integrin activation. <i>Protein and Cell</i> , 2012, 3, 434-440.	11.0	32
20	Crystallization and preliminary X-ray analysis of SNR 141. <i>Science Bulletin</i> , 1997, 42, 957-959.	1.7	0